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BEST AVAILABLE COPY

M G T P A Q I L G F
 ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC
 L L L L F P G T R C
 TTG TTG CTC TTG TTT CCA GGT ACC AGA TGT
 (leader, -20-1)

D I Q M T Q S P S S
 GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC
 L S A S L G Q R V S
 TTA TCT GCC TCT CTG GGA CAA AGA GTC AGT
 L T C
 CTC ACT TGT (fr. 1, 1-23)

R A S Q D I G I N L
 CGG GCA AGT CAG GAC ATT GGT ATT AAC TTA
 H
 CAT (cdr1, 24-34)

T L Q Q E P D G T I
 TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT
 K R L I Y
 AAA CGC CTG ATC TAC (fr2., 35-49)

A T S S L G S
 GCC ACA TCC AGT TTA GGT TCT (cdr2, 50-56)

G V P K R F S G S R
 GGT GTC CCC AAA AGG TTC AGT GGC AGT AGG
 S G S D Y S L T I S
 TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC
 S L E S G D F V A Y
 AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT
 Y C
 TAC TGT (fr3, 57-88)

L Q Y A S S P Y T
 CTA CAA TAT GCT AGT TCT CCG TAC ACG
 (cdr3, 89-97)

F G G G T K L E I K
 TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA
 (fr4, 98-107)

R A D A A P T V S I
 CGG GCT GAT GCT GCA CCA ACT GTA TCC ATC
 F P P S S K L G
 TTC CCA CCA TCC AGT AAG CTT GGG

FIG. 1



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M	E	C	S	W	V	F	L	F	L	L	S	I	T	T	G	V
ATG	GAA	TGC	AGC	TGG	GTC	TTT	CTC	TTC	CTC	CTG	TCA	ATA	ACT	ACA	GGT	GTC
Met	Glu	Cys	Ser	Trp	Val	Phe	Leu	Phe	Leu	Leu	Ser	Ile	Thr	Thr	Gly	Val

H	S
CAC	TCC
His	Ser

(leader)

Q	A	Y	L	Q	Q	S	G	A	E	L	V	R	S
CAG	GCT	TAT	CTA	CAG	CAG	TCT	GGG	GCT	GAG	CTG	GTG	AGG	TCT
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Ser

G	A	S	V	K	M	S	C	K	A	S	G	Y	T	L	T
GGG	GCC	TCA	GTG	AAG	ATG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACA	TTG	ACC
Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Leu	Thr

(1-30, Fr. #1)

S	Y	N	M	H
AGT	TAC	AAT	ATG	CAC
Ser	Tyr	Asn	Met	His

(31-35, CDR 1)

W	V	K	Q	T	P	G	Q	G	L	E	W	I	G
TGG	GTA	AAG	CAG	ACA	CCT	GGA	CAG	GGC	CTG	GAA	TGG	ATT	GGA
Trp	Val	Lys	Gln	Thr	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly

(36-49, Fr. #2)

N	I	F	P	G	N	G	D	T	Y	Y	N	Q	K	F	K	G
AAT	ATT	TTT	CCT	GGA	AAT	GGT	GAT	ACT	TAC	TAC	AAT	CAG	AAG	TTT	AAG	GGC
Asn	Ile	Phe	Pro	Gly	Asn	Gly	Asp	Thr	Tyr	Tyr	Asn	Gln	Lys	Phe	Lys	Gly

(50-66, CDR 2)

K	A	S	L	T	A	D	T	S	S	S	T	A	Y	M	Q
AAG	GCC	TCA	TTG	ACT	GCA	GAC	ACA	TCC	TCC	AGC	ACA	GCC	TAC	ATG	CAG
Lys	Ala	Ser	Leu	Thr	Ala	Asp	Thr	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln

I	S	S	L	T	S	E	D	S	A	V	Y	F	C	A	R
ATC	AGC	AGC	CTG	ACA	TCT	GAA	GAC	TCT	GCG	GTC	TAT	TTC	TGT	GCA	AGA
Ile	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg

(67-98, Fr. #3)

G	N	W	E	G	A	L	D	Y
GGG	AAC	TGG	GAG	GGT	GCT	CTG	GAC	TAC
Gly	Asn	Trp	Glu	Gly	Ala	Leu	Asp	Tyr

(99-107, CDR 3)

W	G	Q	G	T	S	V	T	V	S	S
TGG	GGT	CAA	GGA	ACC	TCA	GTC	ACC	GTC	TCC	TCA
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser

(108-118, Fr. #4)

A	K	T	T	P	P	P	V	Y	P	L	V	P	G	S	L
GCC	AAA	ACG	ACA	CCC	CCA	CCC	GTC	TAT	CCA	CTG	GTC	CCT	GGA	AGC	TTG
Ala	Lys	Thr	Thr	Pro	Pro	Pro	Val	Tyr	Pro	Leu	Val	Pro	Gly	Ser	Leu

(constant region)

FIG. 2

DIQMTQSPSSLSASLGQRVSLTC — Framework #1, 1–23

RASQDIGINLH — CDR-1, 24–34

TLQQEPDGTIKRLIY — Framework #2, 35–49

ATSSLGS — CDR-2, 50–56

GVPKRFSGSRSGSDYSLTISSLESGDFVAYYC — Framework #3, 57–88

LQYASSPYT — CDR-3, 89–97

FGGGTKLEIK — Framework #4, 98–107

FIG. 3A

QAYLQQSGAELVRSGASVKMSCKASGYTLT — Framework #1, 1–30

SYNMH — CDR-1, 31–35

WVKQTPGQGLEWIG — Framework #2, 36–49

NIFPGNGDTYYNQKFKG — CDR-2, 50–66

KASLTADTSSSTAYMQISLTSEDSAVYFCAR — Framework #3, 67–98

GNWEGALDY — CDR-3, 99–107

WGQGTSVTVSS — Framework #4, 108–118

FIG. 3B

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>gb|L41880|MUSIKCC Mus musculus immunoglobulin kappa chain mRNA, 5' end of cds.

```

67 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 126
127 CTCACTTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 186
187 GATGGAAC TATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTGCCCCAAA 246
247 AGGTTCA GTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 306
307 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGGAGGG 366
367 GGGACCAAGCTGGAAATAAAA 387

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>gb|L48667|MUSX Mus musculus (cell line C3H/F2-15) chromosome 6 anti-DNA antibody light chain mRNA.

```

1 GANATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
61 CTCACTTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 120
121 GATGGAAC TTTTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTGCCCCAAA 180
181 AGGTTCA GTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTGTCCGTACACGTTCCGGAGGG 300
301 GGGACCAAGCTGGAAATAAAA 321

```

>gb|J00565|MUSIGKAC1 Mouse ig kappa active gene: vk41 v-j region.

```

313 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 372
373 CTCACTTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 432
433 GATGGAAC TATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTGCCCCAAA 492
493 AGGTTCA GTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 552
553 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGGA 612
613 GGCACCAAGCTGGAAATCAAA 633

```

>emb|V00808|MMIGK7 Part of the murine gene for kappa-immunoglobulin leader peptide and variable part (cell line MOPC41).

```

314 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 373
374 CTCACTTGTCGGCCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 433
434 GATGGAAC TATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTGCCCCAAA 493
494 AGGTTCA GTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 553
554 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGGA 613
614 GGCACCAAGCTGGAAATCAAA 634

```

>gb|I03643|I03643 Sequence 4 from patent US 4642334.

```

1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
61 CTCACTTGTCGGCCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 120
121 GATGGAAC TATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTGCCCCAAA 180
181 AGGTTCA GTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGGA 300
301 GGCACCAAGCTGGAAATCAAA 321

```

>gb|M59920|MUSIGKAA3 Mouse IG germline chain mRNA V-J region, partial cds.

```

1 ATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTC 60
61 ACTTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCAGAC 120
121 GGAAC TATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTGCCCCAAAAGG 180
181 TTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAA 240
241 GATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGAGGC 300
301 ACCAAGCTGGAAATCAAA 318

```

FIG. 4A

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>gb|M36246|MUSIGLAFA Mouse Ig kappa-chain mRNA V region, partial cds, from
hybridoma H220-23.

```

1 TCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCTGGGCAAGT 60
61 CAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCAGATGGAACATTAAACGC 120
121 CTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGGTTTCAGTGGCAGTAGG 180
181 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGTAGACTAT 240
241 TACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGGGGGACCAAGCTGNAAATA 300
301 AAA 303

```

>emb|Z22118|MDIGKVBS M.domesticus IgK variable region.

```

1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
61 CTCACCTTGTCTGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 120
121 GATGGAACATTAAACGCCTGATCTACAGCACATCCACTTTAAATTCTGGTGTCCCCAAA 180
181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
241 GAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGG 300
301 GGGACCAAACCTGGAAATAAAA 321

```

>gb|M64168|MUSIGKFT Mouse Ig active kappa-chain mRNA V-region.

```

4 TCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCTGGGCAAGT 63
64 CAGGACATTGGTAATAGCTTAAACTGGCTTCAGCAGGAACCAGATGGAACATTAAACGC 123
124 CTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGGTTTCAGTGGCAGTAGG 183
184 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAATCTGAAGATTTTGTAGTCTAT 243
244 TACTGTCTACAATATGCTAGTTATACGTACACGTTTCGGAGGGGGGACCAAGTTGGAACCTA 303
304 AAA 306

```

>emb|X02177|MMIGGVJ1 M.musculus mRNA for IgG kappa light chain(partial)
Cloop 1

```

42 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 101
102 CTCACCTTGTCTGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 161
162 GATGGAACATTAAACGCCTGATCTACGCCGCATCCACTTTAGATTCTGGTGTCCCCAAA 221
222 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 281
282 GAAGATTTTGCAGACTATTACTGTCTACAATATCTTAGTTATCCGCTCACGTTTCGGTGCT 341
342 GGGACCAAGCTGGAGCTGAAA 362

```

FIG. 4B

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>gb|L48668|MUSY Mus musculus (cell line C3H/F2-20) chromosome 12 anti-DNA antibody heavy chain mRNA.

```

1 CAGGCTTATNTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 60
61 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
121 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 180
181 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240
241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294
295 ----- 311
312 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357

```

>gb|L48680|MUSAL Mus musculus (cell line C3H/F2-3) chromosome 12 anti-DNA antibody heavy chain mRNA.

```

1 CAGGCTTATGTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 60
61 TCCTGCAAGGCTTCTGGCTACAGATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
121 CGTAGACAGGGCCTGGAATGGATTGGAGCAATTTATCCAGGAAATGGTGATACTTCCTAT 180
181 AATCAGAAGTTCAAGGGCAAGGCCACACTGATTGTAGACAAATCCTCCAGCACAGCCTAC 240
241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGAGA 298
299 GGGGTAACACTAGTAGGACATATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 357
358 TCA 360

```

>emb|X64805|MMAIDHCH M.musculus mRNA for anti-Id mAB 114 heavy chain, variable region.

```

1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTAAGGCCTGGGTCCTCAGTGAAGATG 60
61 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
121 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 180
181 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240
241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGGAT 300
301 TACTCCGGTAGTATAGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 354

```

>gb|M17953|MUSIGHXW Mouse Ig rearranged H-chain V-region mRNA VJ1.

```

96 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 155
156 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 215
216 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 275
276 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 335
336 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGTG 392
393 ----- 427
428 CTGGGGCACAGGGACCACGGTCACCGTCTCC 458

```

>gb|I05921|I05921 Sequence 37 from patent EP 0274394.

```

96 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 155
156 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 215
216 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 275
276 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 335
336 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGTG 392
393 ----- 427
428 CTGGGGCACAGGGACCACGGTCACCGTCTC 457

```

FIG. 5A

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>emb|Z22117|MDIGGVBC M.domesticus IgG variable region.

```

  2 AGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATAT 61
 62 CCTGCAAGGCTTCTGGATACACATTCAGTACTACTACATGCACTGGGTGAAGCAGAAGC 121
122 CTGGGCAGGGCCTTGAGTGGATTGGAGAGATTTATCCTGGAAGTGGTAATACTTACTACA 181
182 ATGAGAAGTTCAAGGGYAAGGCCTCACTGACTGCAGACAAATCCTCCAGCACAGCCTACA 241
242 TGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTTCTGTGCAAGACGTTACT 301
302 ----- 314
315 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

```

>gb|M15224|MUSIGLAF Mouse IgM H-chain lambda rearranged anti-Dns hybridoma VDJ4 region of J558 family mRNA.

```

  1 CAGGTTTCAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60
 61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAAACAGAGG 120
121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTTATCCTGGAGATGGTGATACTAGGTAC 180
181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCCTCCAGCACAGCCTAC 240
241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAG 295
296 ----- 314
315 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

```

>gb|M15226|MUSIGLAH H-chain lambda rearranged anti-Dns hybridoma VDJ4 region of J558 family mRNA.

```

  1 CAGGTTTCAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60
 61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAAACAGAGG 120
121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTTATCCTGGAGATGGTGATACTAGGTAC 180
181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCCTCCAGCACAGCCTAC 240
241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 294
295 ----- 317
318 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 363

```

>gb|M15225|MUSIGLAG H-chain lambda rearranged anti-Dns hybridoma VDJ4 region of J558 family mRNA.

```

  1 CAGGTTTCAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60
 61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAAACAGAGG 120
121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTTATCCTGGAGATGGTGATACTAGGTAC 180
181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCCTCCAGCACAGCCTAC 240
241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 294
295 ----- 311
312 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357

```

>gb|M20835|MUSIGKCLP Mouse IgMk rearranged heavy-chain mRNA variable region (V-D-J) anti-DNA autoantibody.

```

106 CAGGTCCAACCTGCAGCAGCCTGGTGCTGAGCTTGTGAAGCCTGGGGCCTCAGTGAAGCTG 165
166 TCCTGCAAGGCTTCTGGCTACACTTTCACCAGCTACTGGATAAACTGGGTGAAGCAGAGG 225
226 CCTGGACAAGGCCTTGAGTGGATTGGAAATATTTATCCTGGTAGTAGTACTAACTAC 285
286 AATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACACATCCTCCAGCACAGCCTAC 345
346 ATGCAGCTCAGCAGCCTGACATCTGACGACTCTGCGGTCTATTATTGTGCAAGACG 401
402 ----- 416
417 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 462

```

FIG. 5B

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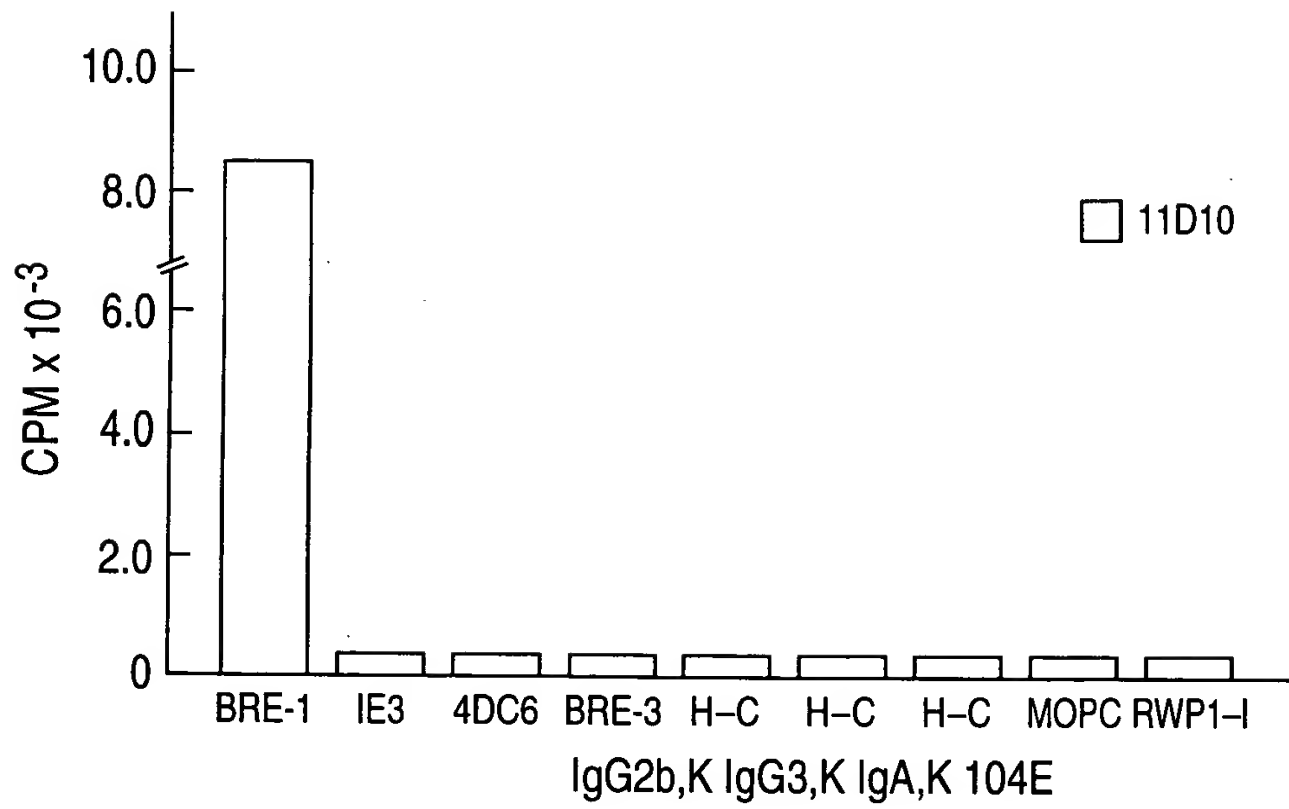


FIG. 6

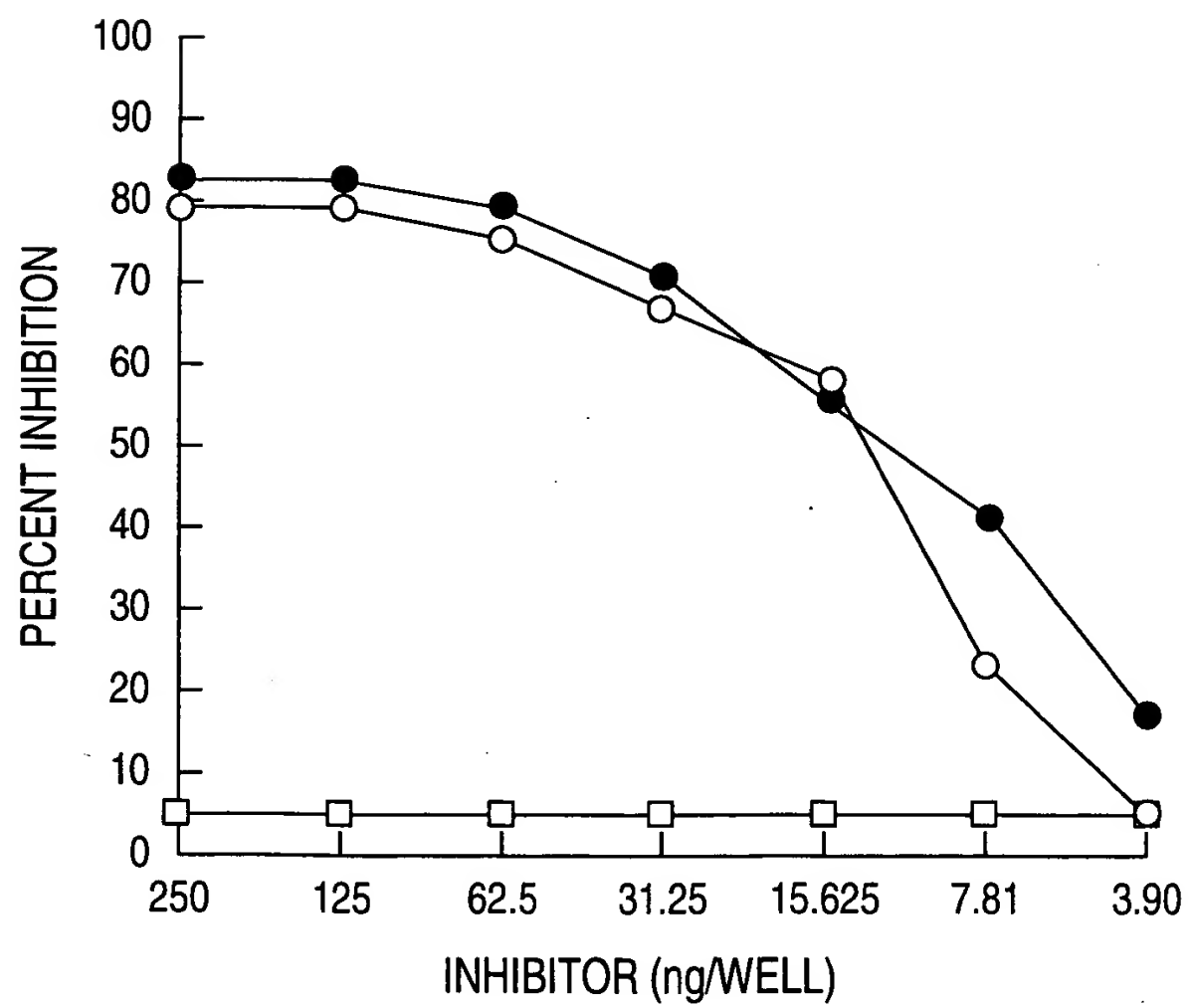


FIG. 7

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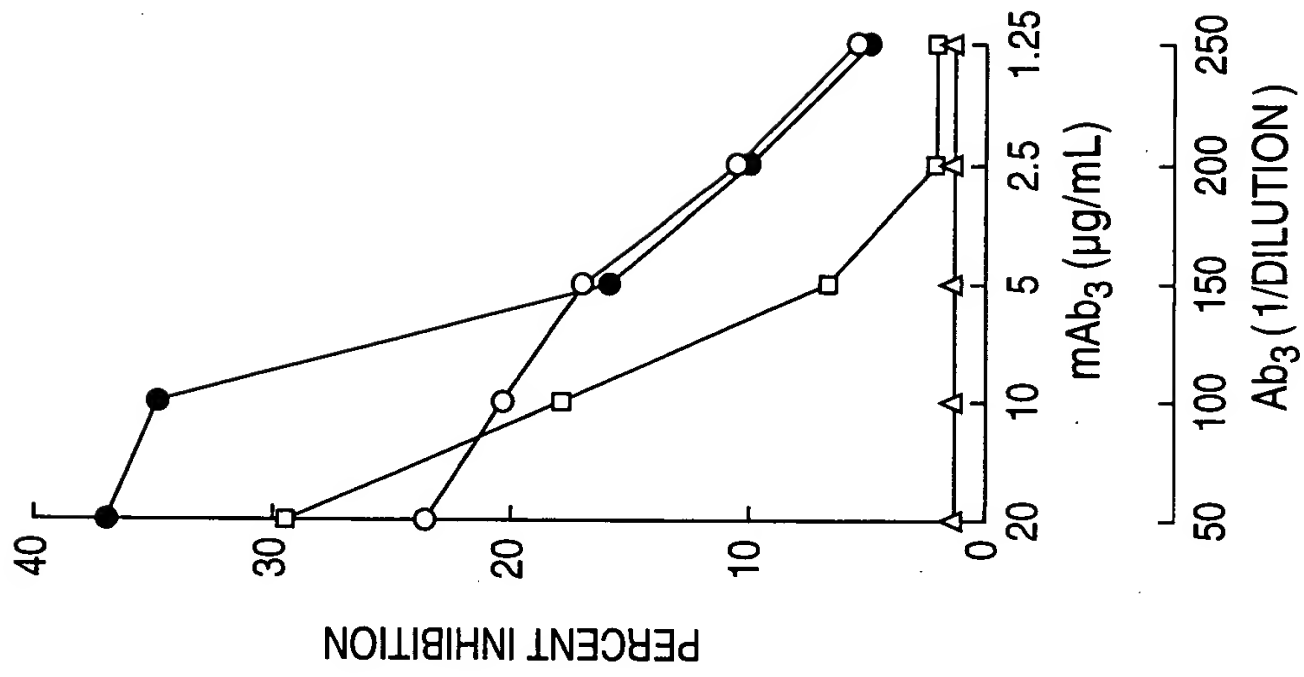


FIG. 9

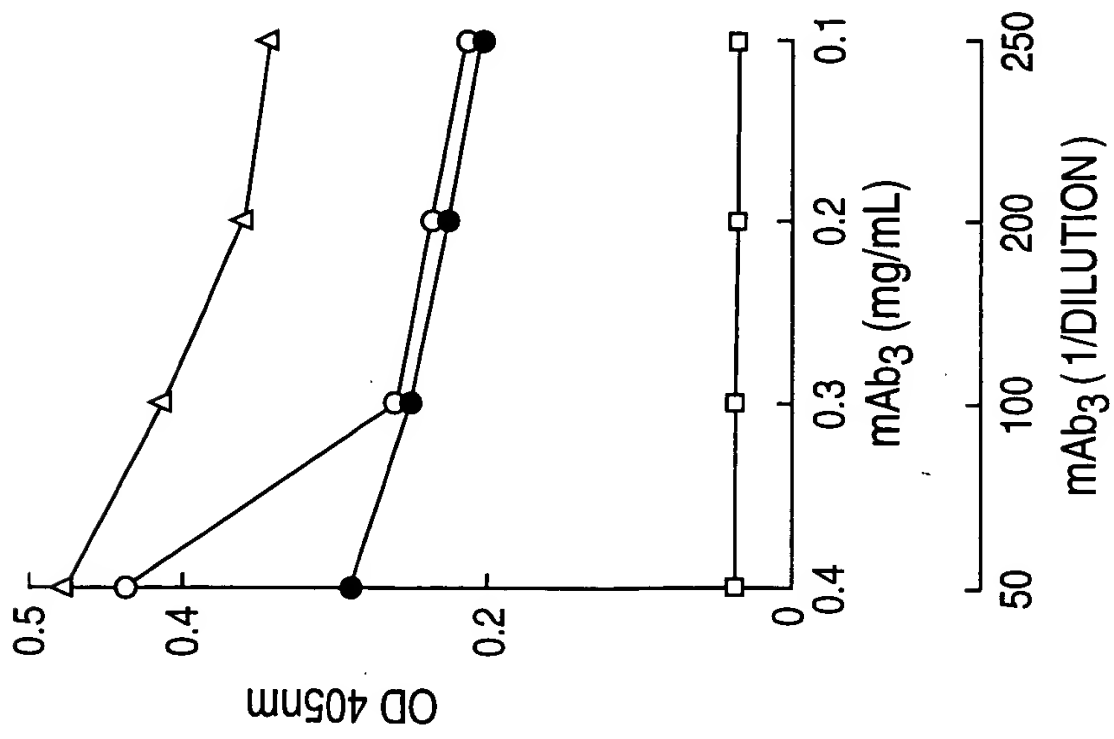


FIG. 8

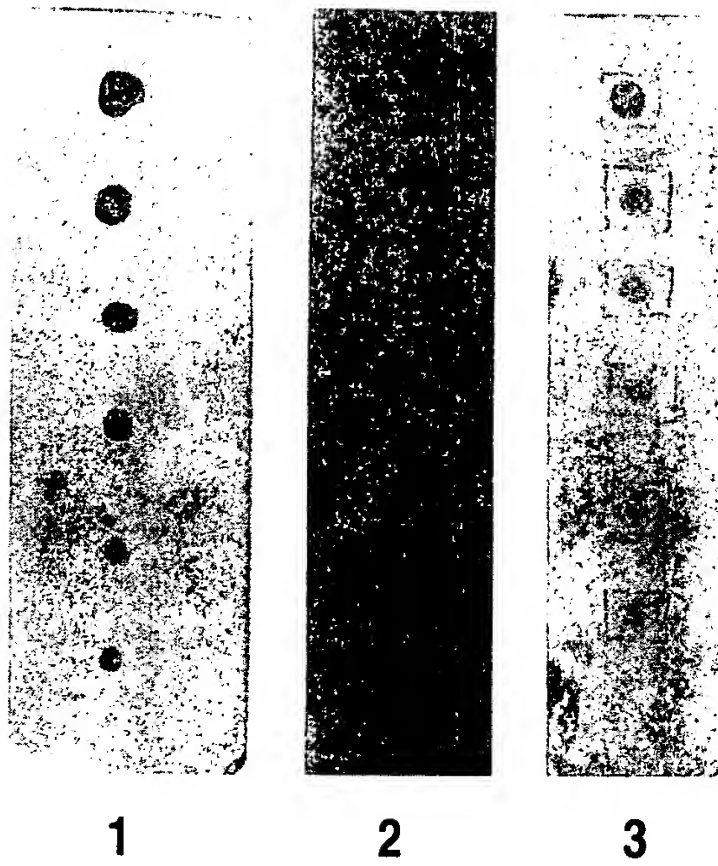


FIG. 10

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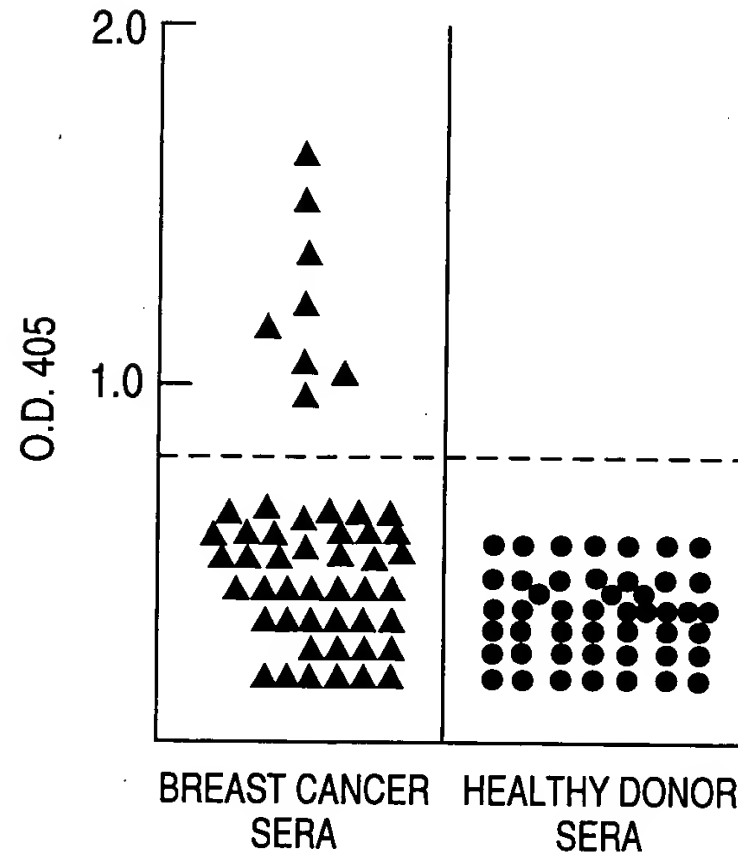


FIG. 11

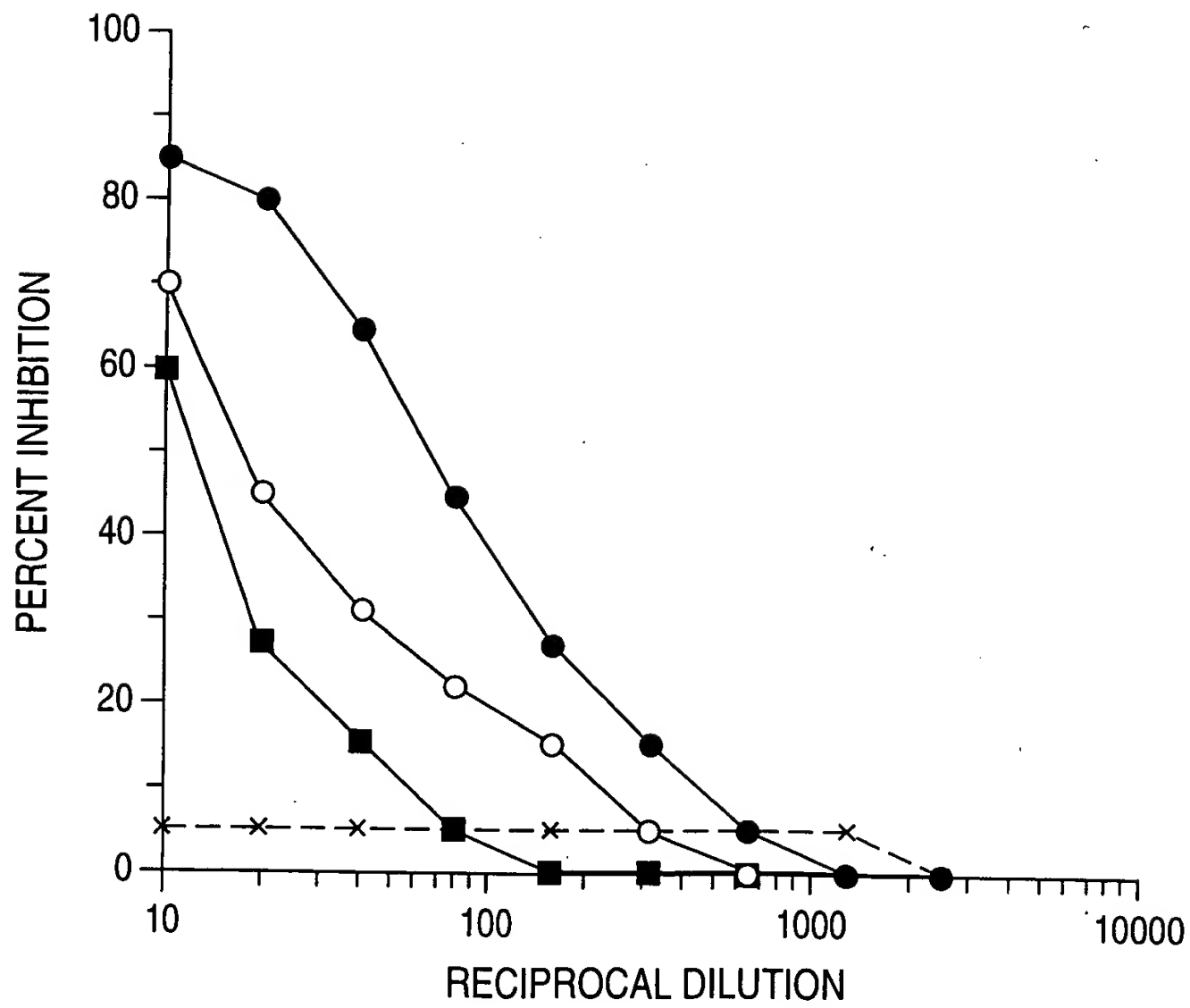


FIG. 12

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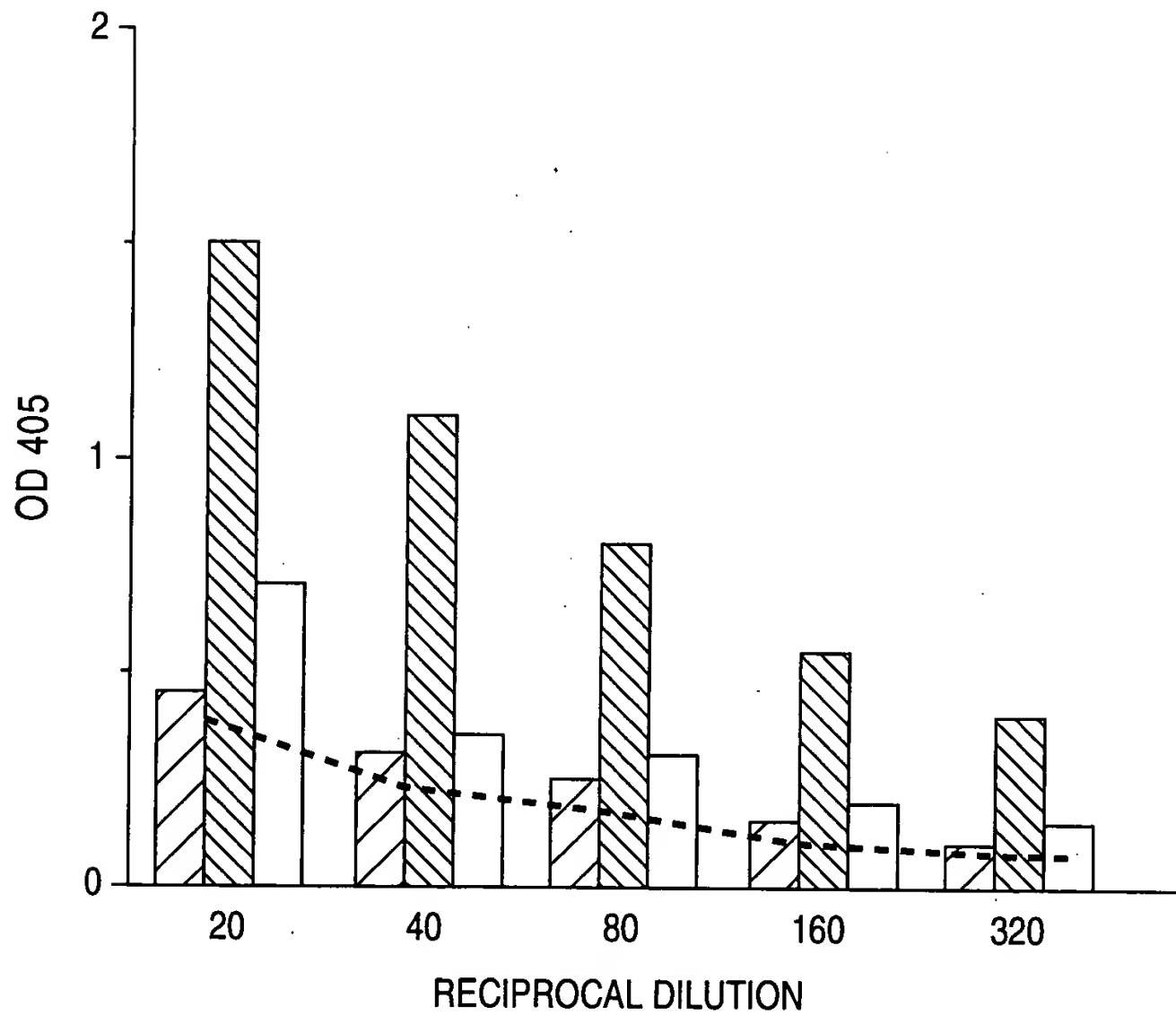


FIG. 13

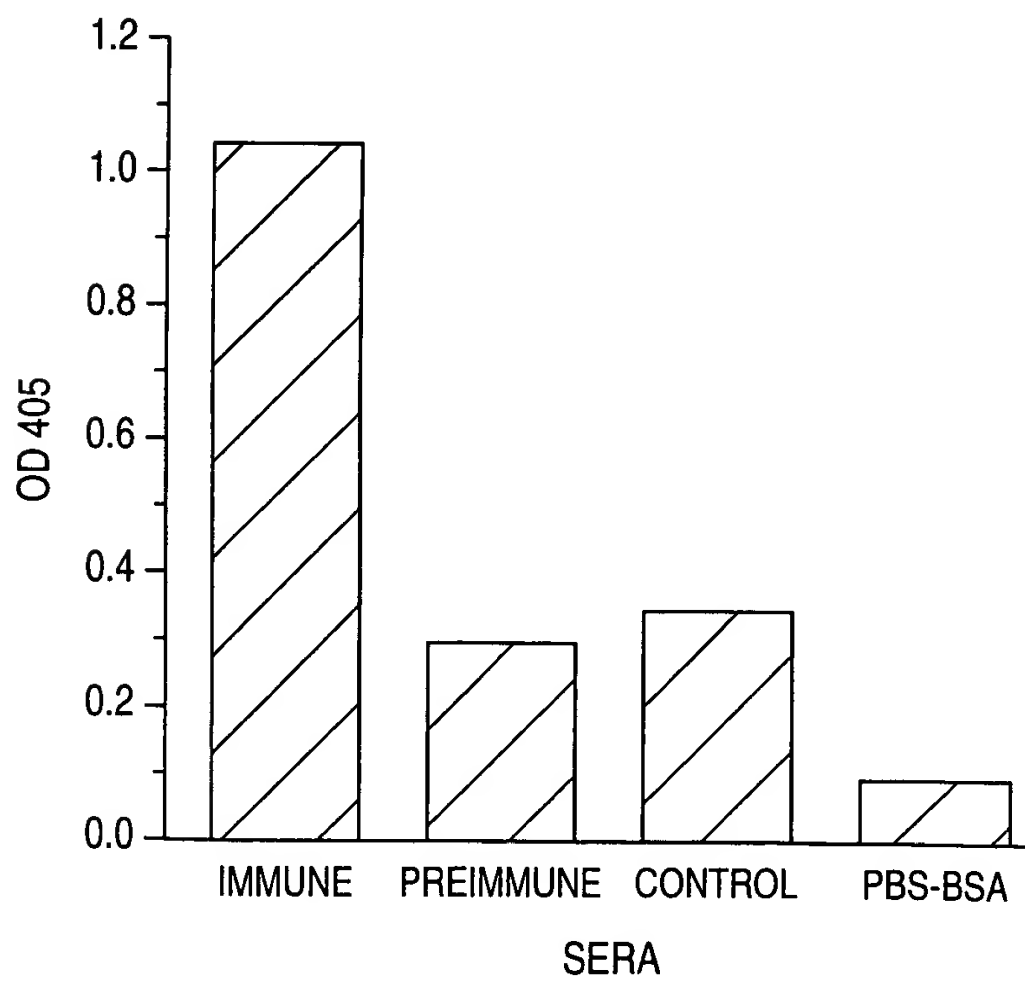


FIG. 14

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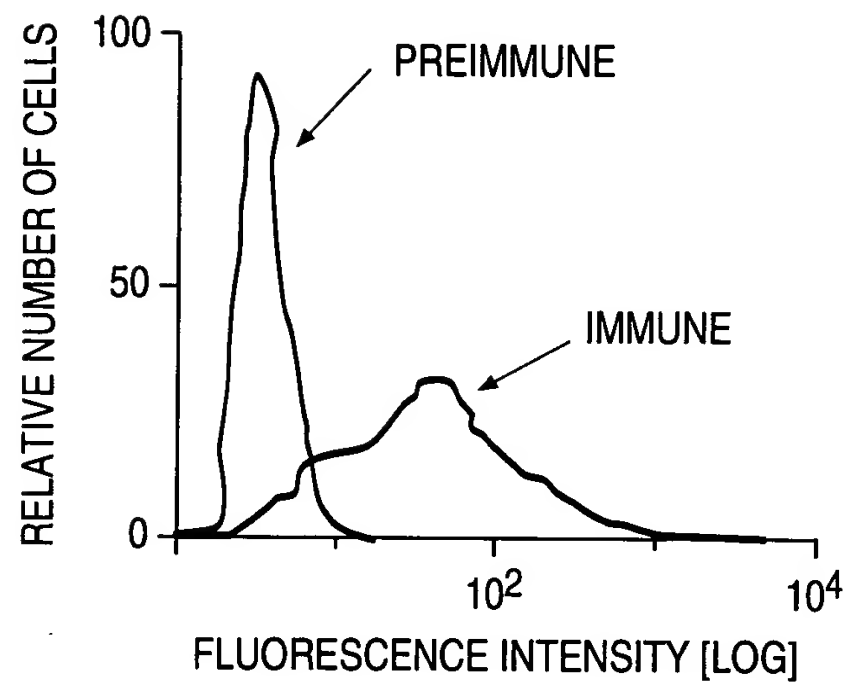


FIG. 15A

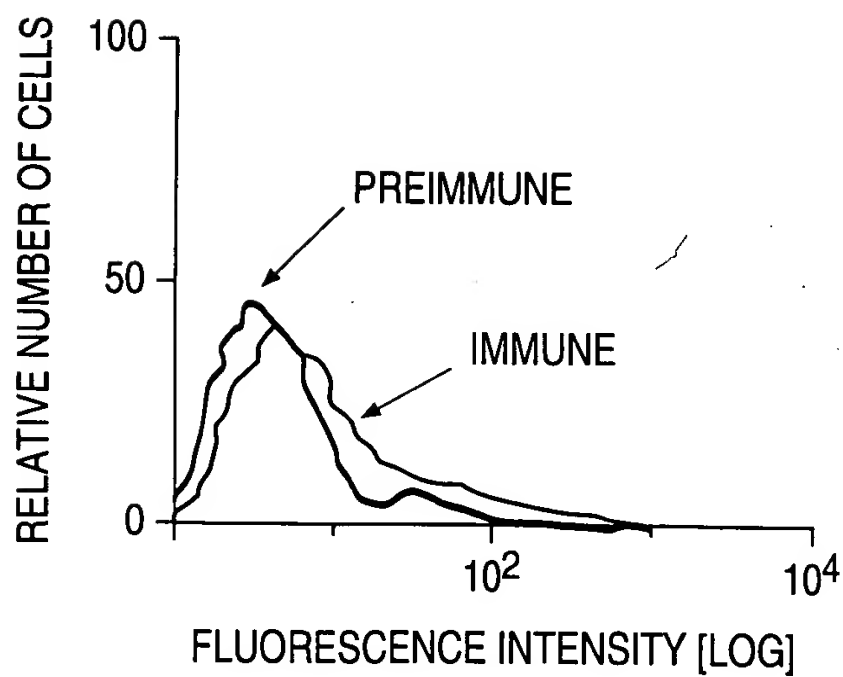


FIG. 15B

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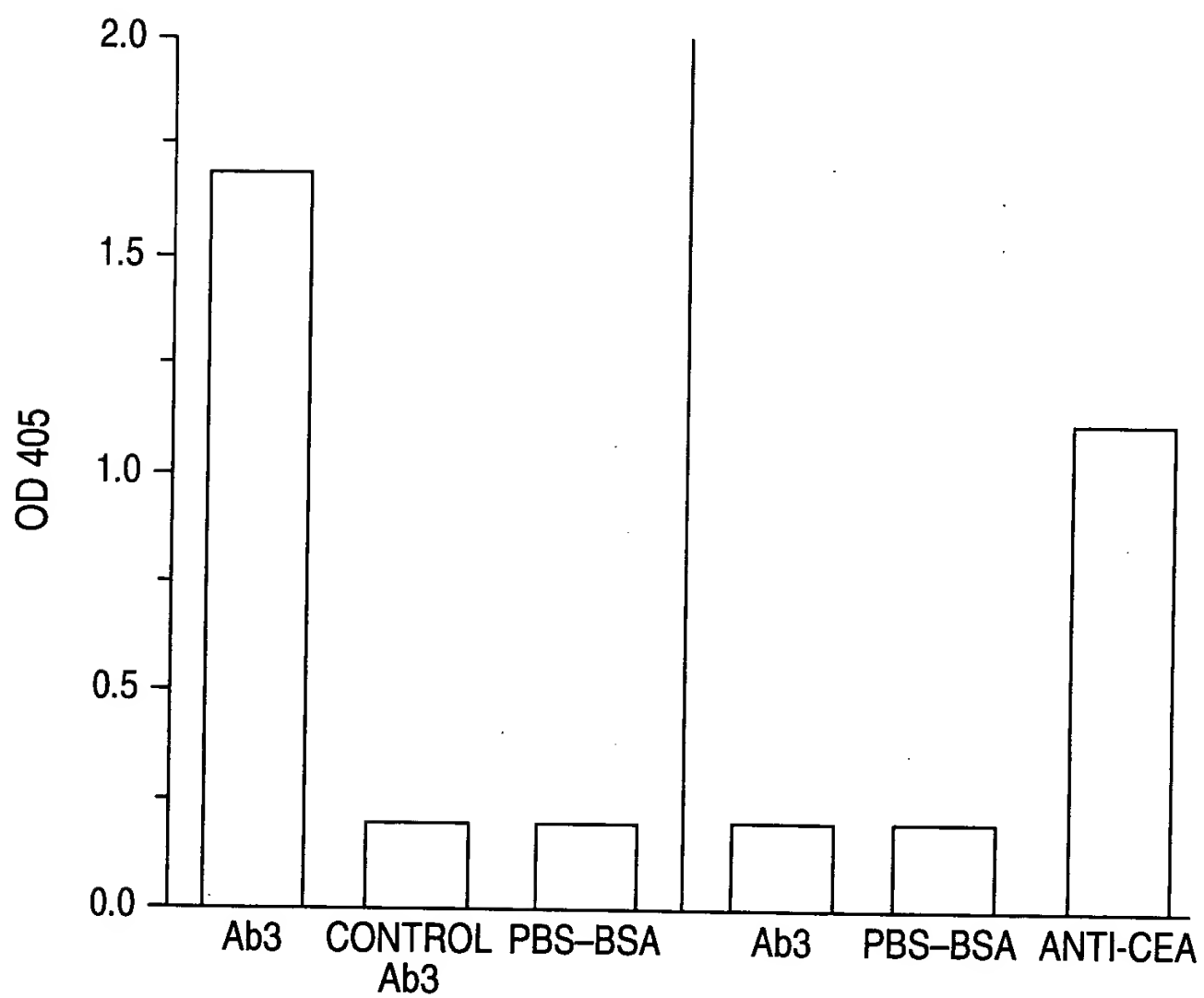


FIG. 16

App No.: 08/766,350

Docket No.: 304142000321

Inventor: Malaya CHATTERJEE et al.

Title: MURINE ANTI-IDIOTYPE ANTIBODY 11D10 AND
METHODS OF USE THEREOF (AS AMENDED)

REPLACEMENT SHEET

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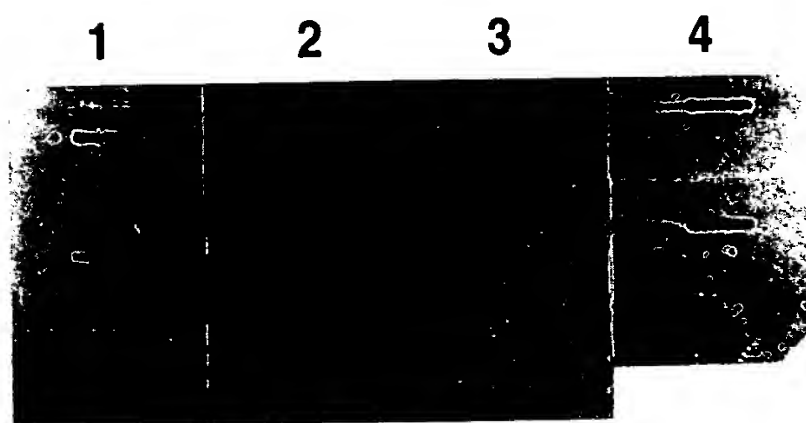


FIG. 17

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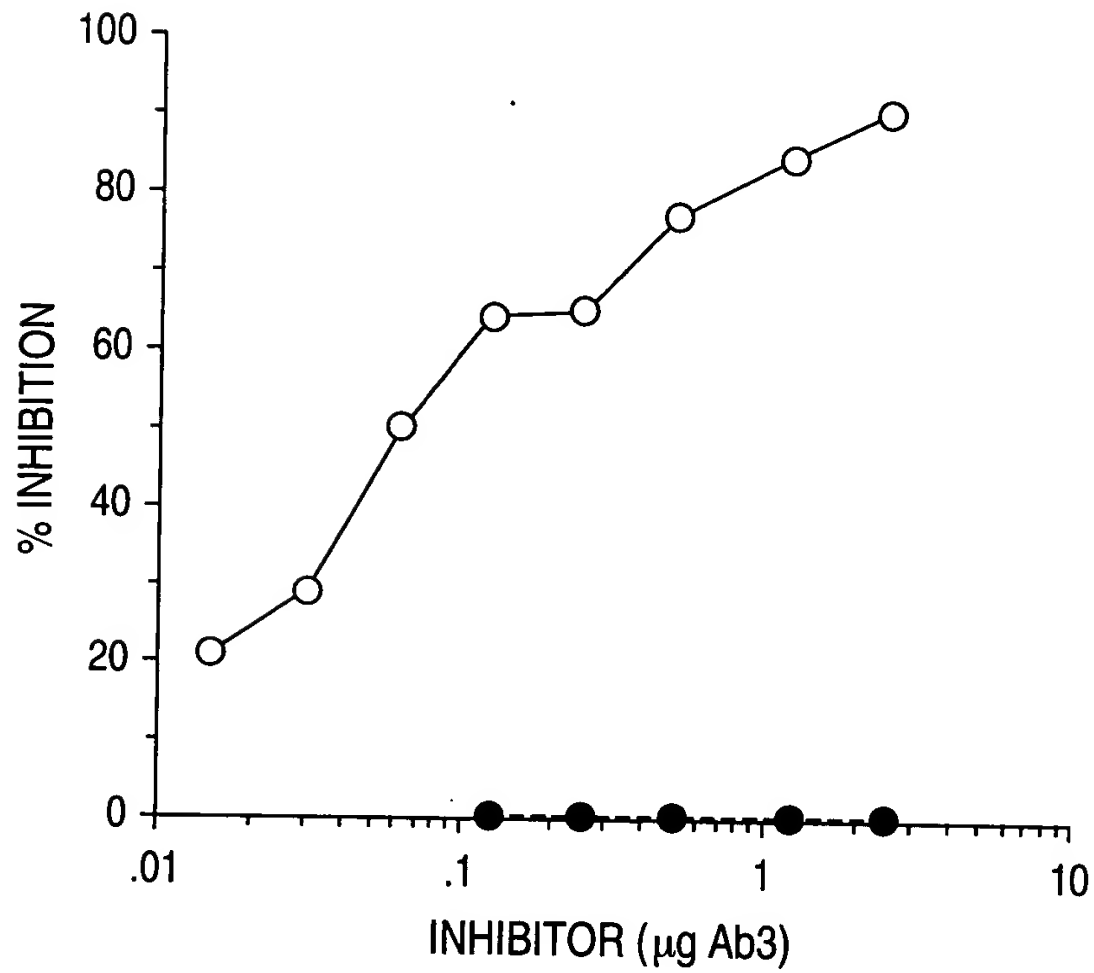


FIG. 18

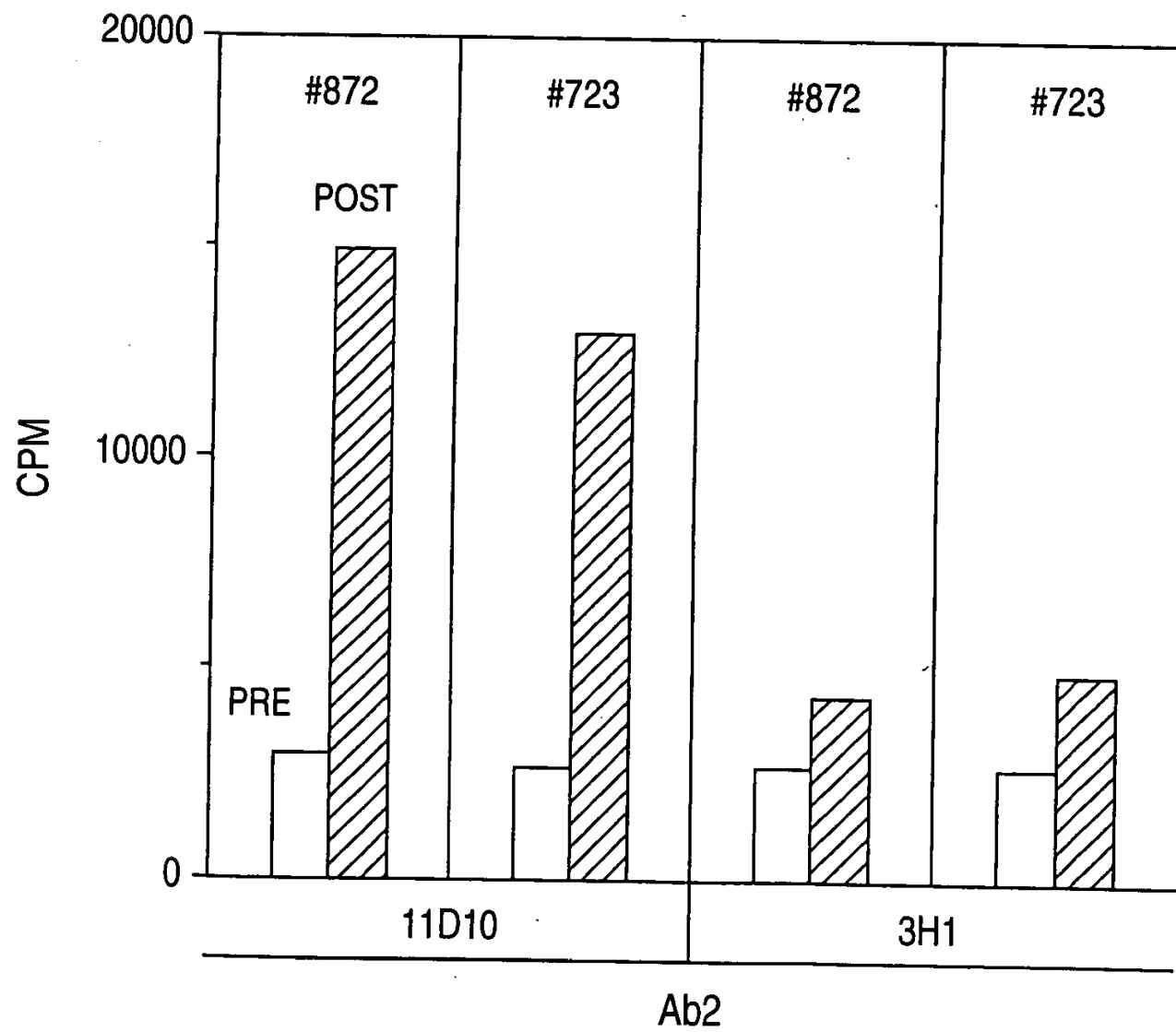


FIG. 19

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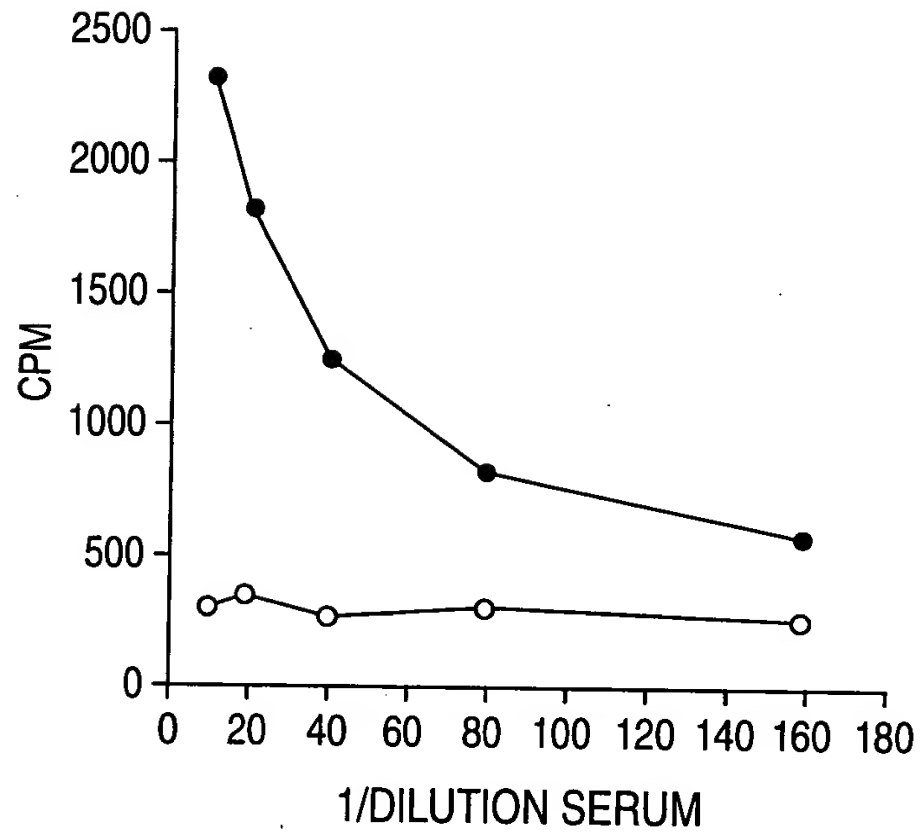


FIG. 20

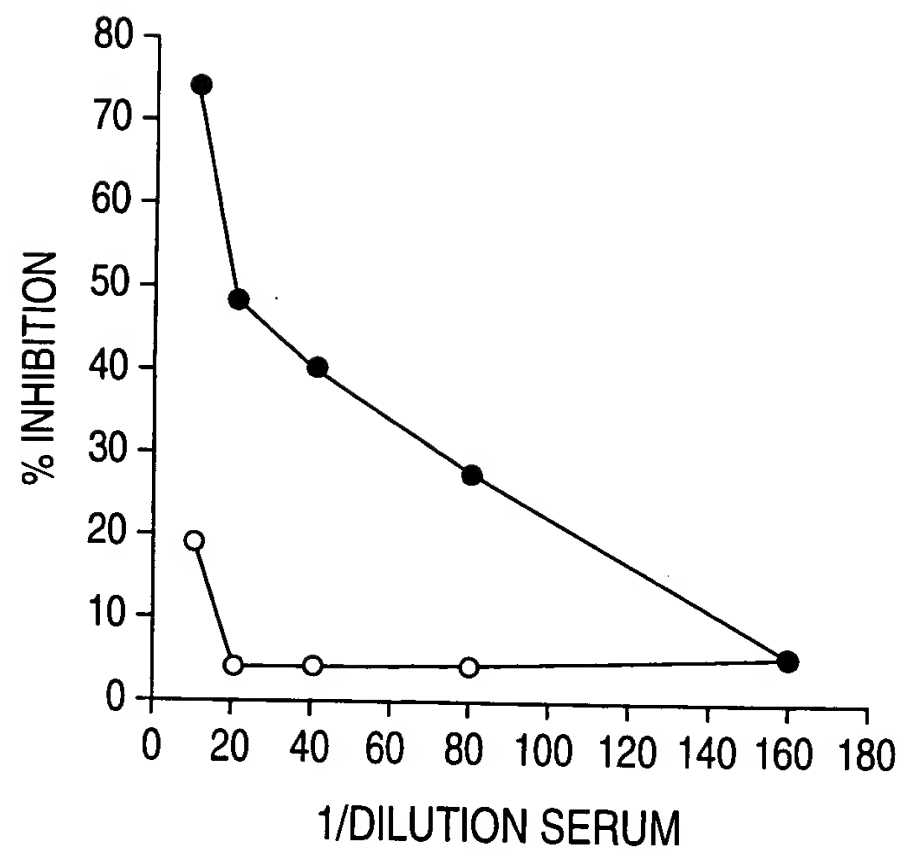


FIG. 21

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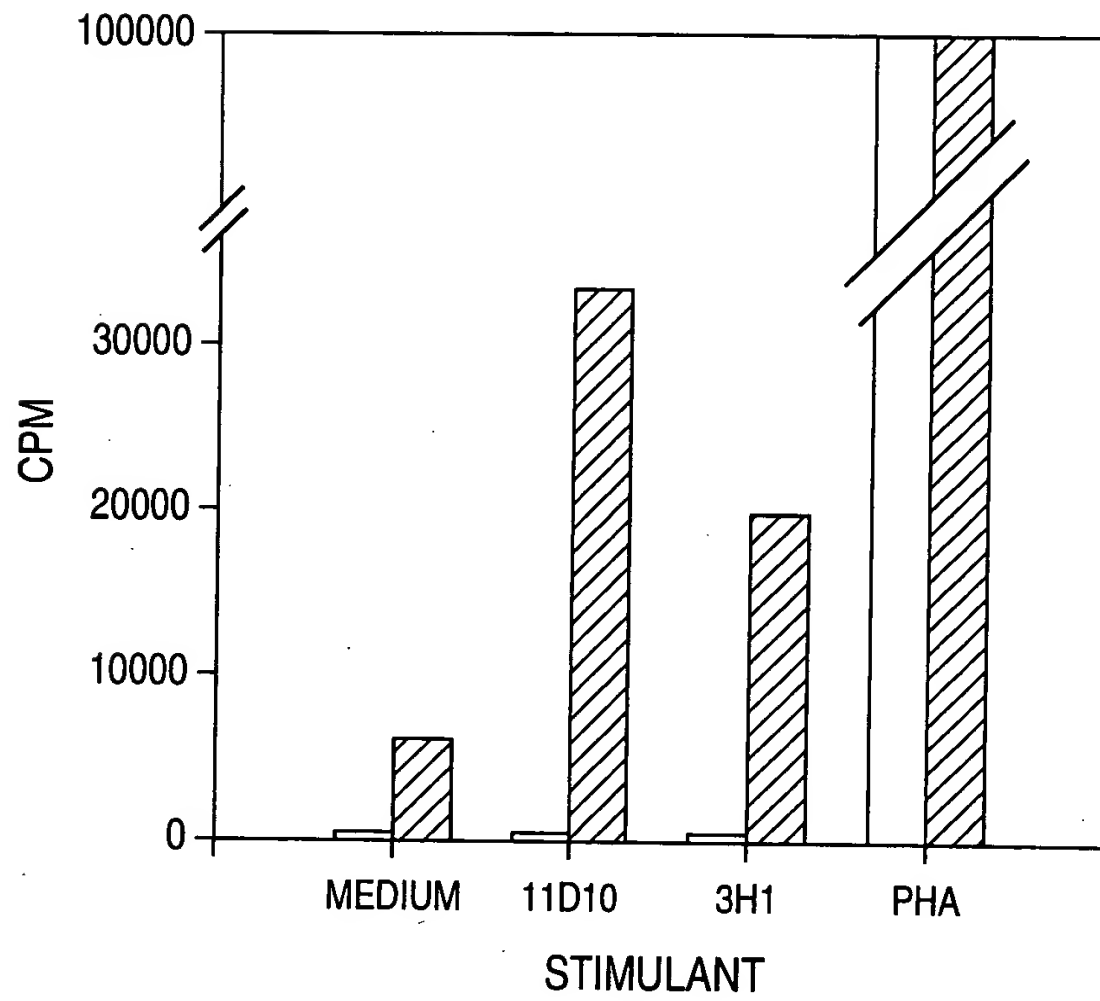


FIG. 22

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Q G L E W I G <u>N I F P G N G D T Y Y N O</u>	V _H (NEAR CDR 2)
: : : :	
R E S P	
G S T A P P A H G V T S A P D T R P A P	HMFG REPEAT (DIRECT)
: : :	
D G T I K R L I Y <u>A T S S L G S</u> G V P L	V _L (NEAR CDR 2)
P S E R P	
P A P R T D P A S T V G H A P P A T S G P A P	HMFG REPEAT (REV.)
: : : : : : : : :	
H T L Q Q E P D G T I K R L I Y <u>A T S S L G S</u>	V _L (NEAR CDR 2)
: : : : :	
A Y Y C <u>L O Y A S S P Y T</u> F G G G T K L E I K	V _L (NEAR CDR 2)

FIG. 23

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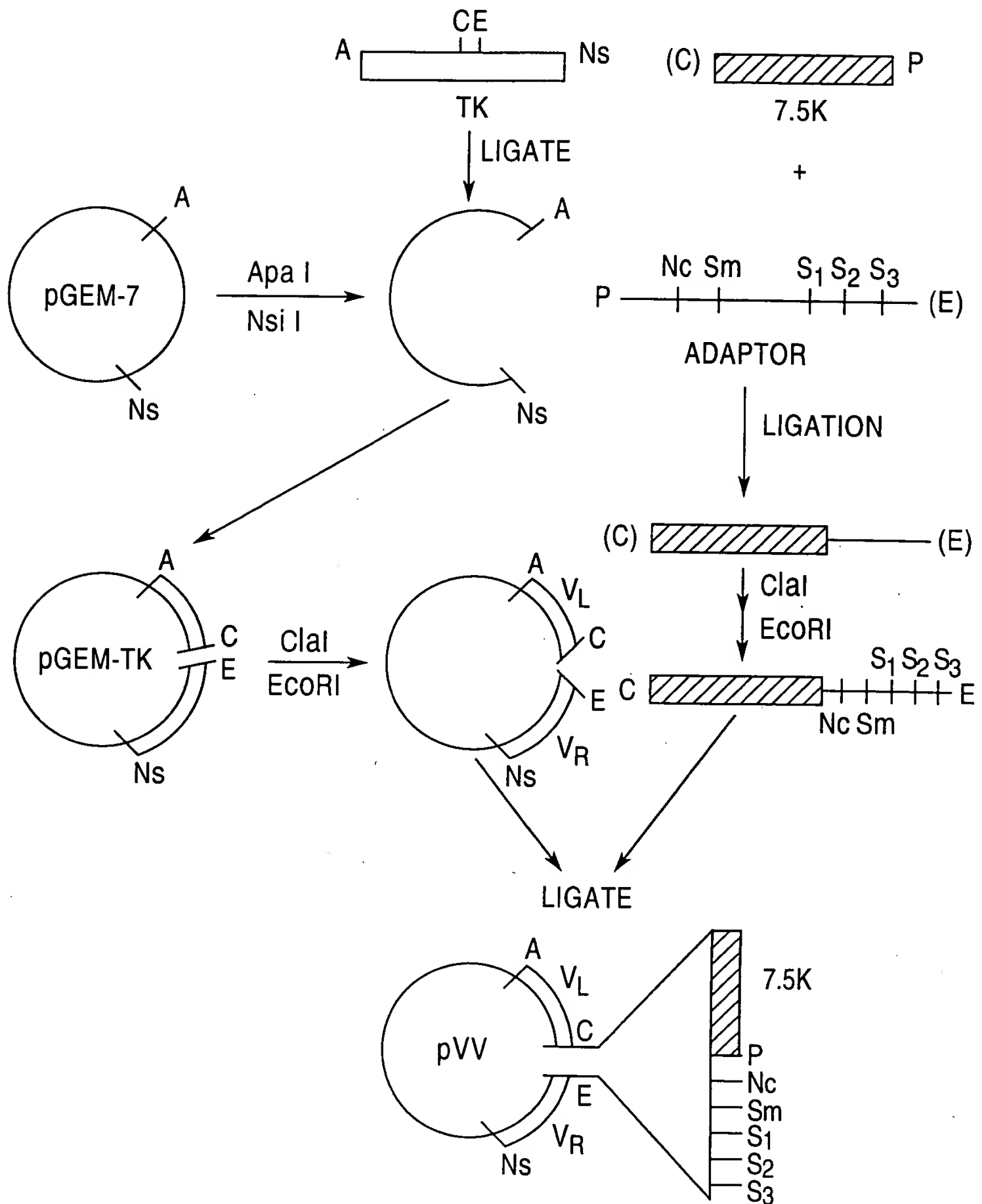


FIG. 24

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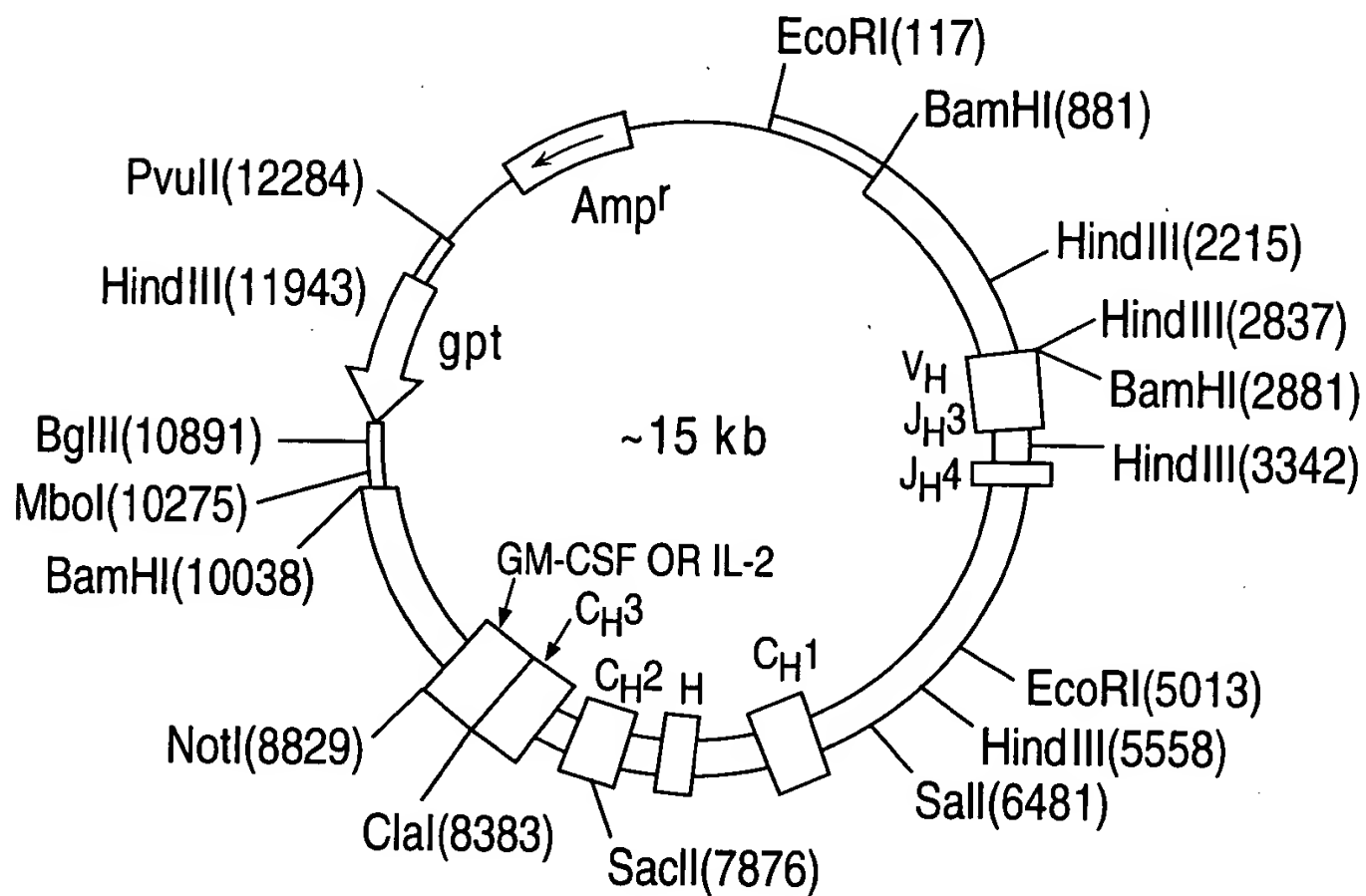


FIG. 25A

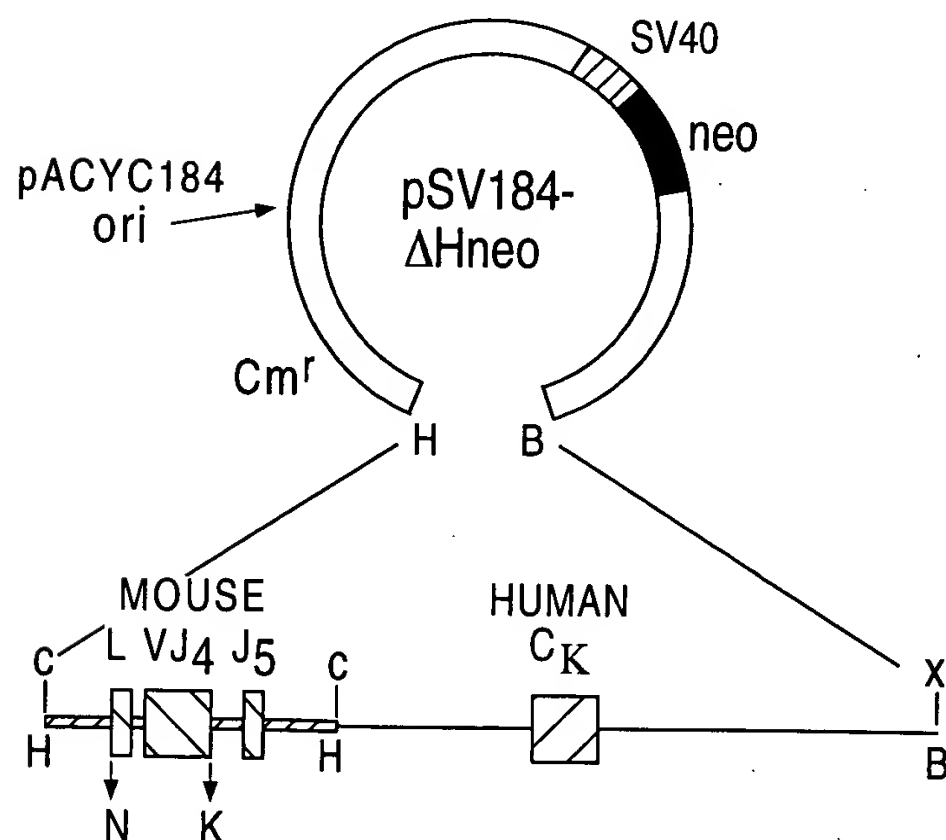


FIG. 25B

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11D10: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60

1	23E.....SS.NW.....D.....	82
2	23E.....SS.NW.....D.....	82
3	23E.....SS.NW.....D.....	82
4	23E.....P.....SS.NW.....D.....	82
5	1E.....SS.NW.....D.....	60
6	1E.....SS.NW.....D.....	59
7	1E.....RS.NW.....D.....	60
8	1E.....E.SGY.SW...K.....S..T.N.....	60
9	1E.....SS.NW.....D.....	54
10	1E.....E.SGY.SW...K.....A.T.D.....	60
11	1	X.....E.....NS.NW.....D.....	55
12	1E.....A.....E..GY.SW...K.....A.T.D.....	60
13	14E.....E.SGY.SW...K.....A.T.D.....	73
14	1	EL.....E.....E.SGY.SW...K.....A.T.D.....	60
15	2	ELVL.....E.....E.NGY.GW...K.....A.T.H.....	61

11D10: 61 RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIK 107

1	83D.....	129
2	83D.....W.....	129
3	83D.....W.....	129
4	83D.....W.....	129
5	61D.....W.....	106
6	60D.....W.....	106
7	61D.....T..W.....	106
8	61AD.....	107
9	55D.....X..	107
10	60AD.....	106
11	56V.....YT.....L.	102
12	61	..G.....AD.....Y.W.....	106
13	74AD.....L.Y.L...A.....L.	120
14	61AD.....Y.L...A.....L.	107
15	62AD.....Y.R.....	108

FIG. 26A

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11D10: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60

1	1P.S.....F.....R.....A.Y.....S.	60
2	20P.....F.....R.....A.Y.....S.	79
3	1	EVQ.....P...KP.....I.....F.D.Y.....K.....E.Y..S.N...	60
4	1	.IQ.....P....P.....I.....F.D.YI.....R..E.....W.Y..S.N.K.	60
5	1	.VQ.....P...KP.....L.....F.D.TI.....S.....W.Y..S.N.K.	60
6	1	.VQ..E.....KP.....L.....F...W.....R.....K.N.S..R.N.	60
7	20	.VQ.....AKP.....F.A.W.....R.....Y.N.NT.Y.E.	79
8	1	EVQ.....KP.....L.....F...W.....R.....E.D.SDSY...	60
9	1	.VQ....E...A.P.....F.R.W.....R...A.....A.Y...S..N.	60
10	1	.VQ.....P.T...I.....F.N.WLG....R..H.....D.Y..G.Y.N.	60
11	20	.VQ.....AKP.....F...R.....R.....Y.N.ST.Y.E.	79
12	1	.VQ.....AKP.....F...W.....R.....Y.N.ST.Y.E.	60
13	1	.IQ.....P....P.....I.....F.D.YI.....R..E.....W.Y..S.N.K.	60
14	1	.VQ.....P.T.....A...F.N.WIG....R..H.....D.Y..G.Y.N.	60
15	1	EVQ.....TV.A.P.....F...W.....R.....A.Y...S..R.	60

11D10: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG=NWEG=ALDYWGQGTSVTVSS 118

1	61T..V.K.....L.....=DYS.=SI.....TL....	118
2	80T..V.K.....L.....xxxxxxxxxx=xx.V..T..T....	140
3	61	.E.....K.....L.....xxxxxxxxx=.M.....	120
4	61	.E.....T..V.....L.....=xxx=.M.....	117
5	61	.D.....TM...K.....L.....=VAR.S=.M.....	119
6	61	.E...S..T..V.K.....L.....Y...xxxxxxxxx.....T.....	123
7	80	..N..D..T...K.....L.....Y.T.xxx.Y..=.M.....	139
8	61T..V.K.....F.....Y...xxxxxxxxx=xM.....	120
9	61K...V..A....EL...A.....Y...S=R.YR.=SM.....	119
10	61	.E.....T.....L.....P=HYY.=SG.....TL....	118
11	80D..T...K.....L...F.....Y....=x.=VF.....TL....	135
12	61D..T...K.....L.....L.Y...W=VYYY=.M.....	118
13	61	.E.....T..V.....L.....=xxx=.M.....	117
14	61	.E.....T.....L.....I.Y...P=FYFY=.M.....C....	118
15	61K...V..A....EL...N.....Y.T..=GLFT=.M.....	115

FIG. 26B

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Light Chain

```
*****  
*****  
VL consensus: 1 DIQMTQSPSSLSASLGERSVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGV PK 60  
11D10: 1 .....Q.....IN.HT.....G..... 60
```

HMFG fragments: GSIAPPAHRVTSAPESRPPP
ppprsepastvrhappatsg

```
*****  
VL consensus: 61 RFSGSRSGSDYSLTISSLESGDFVDYYCLQYASSPYTFGGGTKLEIK 107  
11D10: 61 .....A..... 107
```

HMFG fragments: ppprsepastvrhappatsg

Heavy Chain

```
*****  
*****  
VH consensus: 1 QVQLQQSGAELVRPGASVKMSCKASGYTFTSYWMHWVKQRPGQGLEWIGAIYPGNGDTNY 60  
11D10: 1 .AY.....S.....L...N.....T.....N.F.....Y. 60
```

HMFG fragments: APDIRPPP

```
*****  
*****  
VH consensus: 61 NQKFKGKATLTADTSSSTAYMQLSSLTSEDSAVYFCARGxxxGAMDYWGQGTSTVTVSS 118  
11D10: 61 .....S.....I.....NWE..L..... 118
```

FIG. 26C

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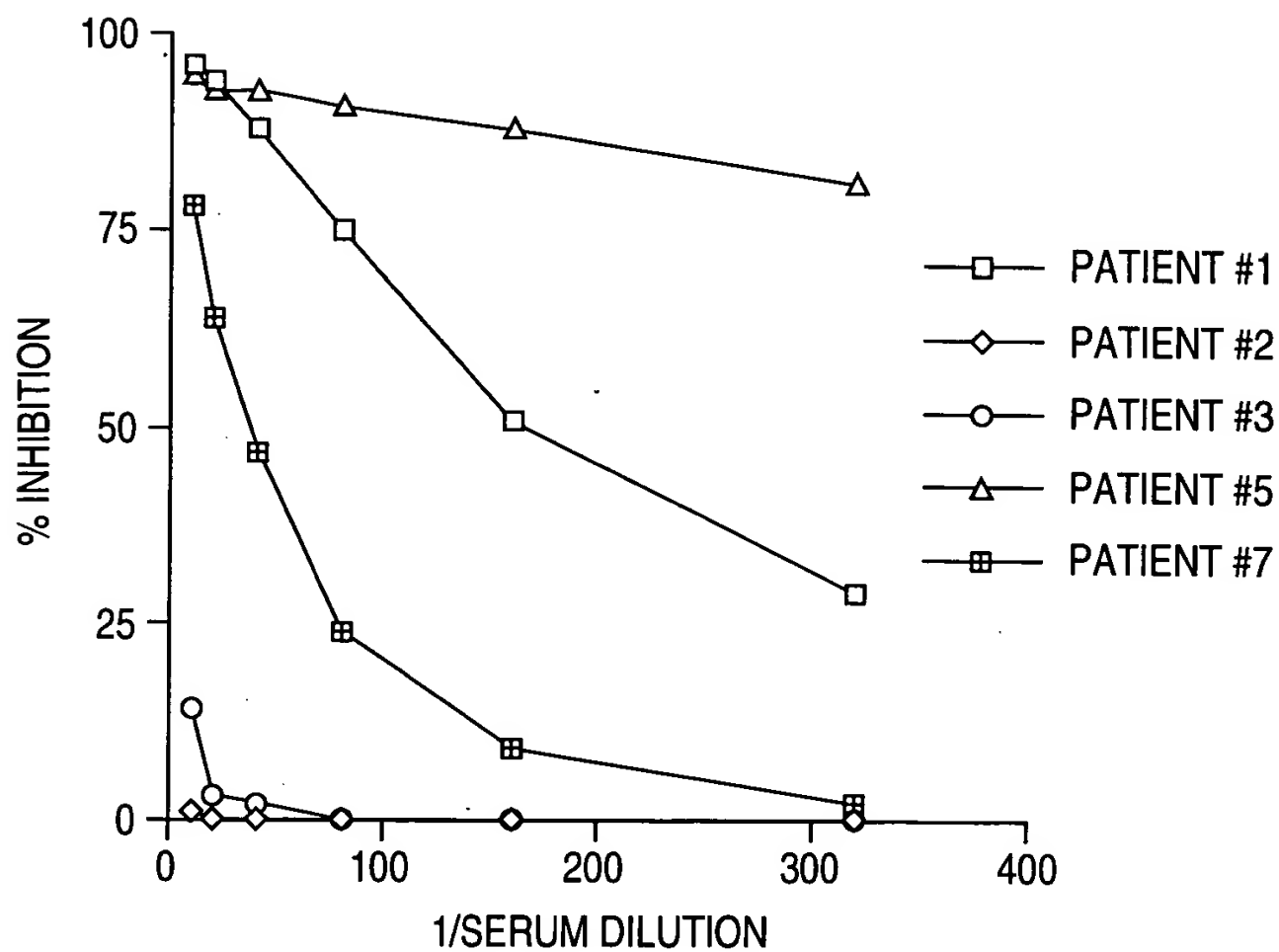


FIG. 27A

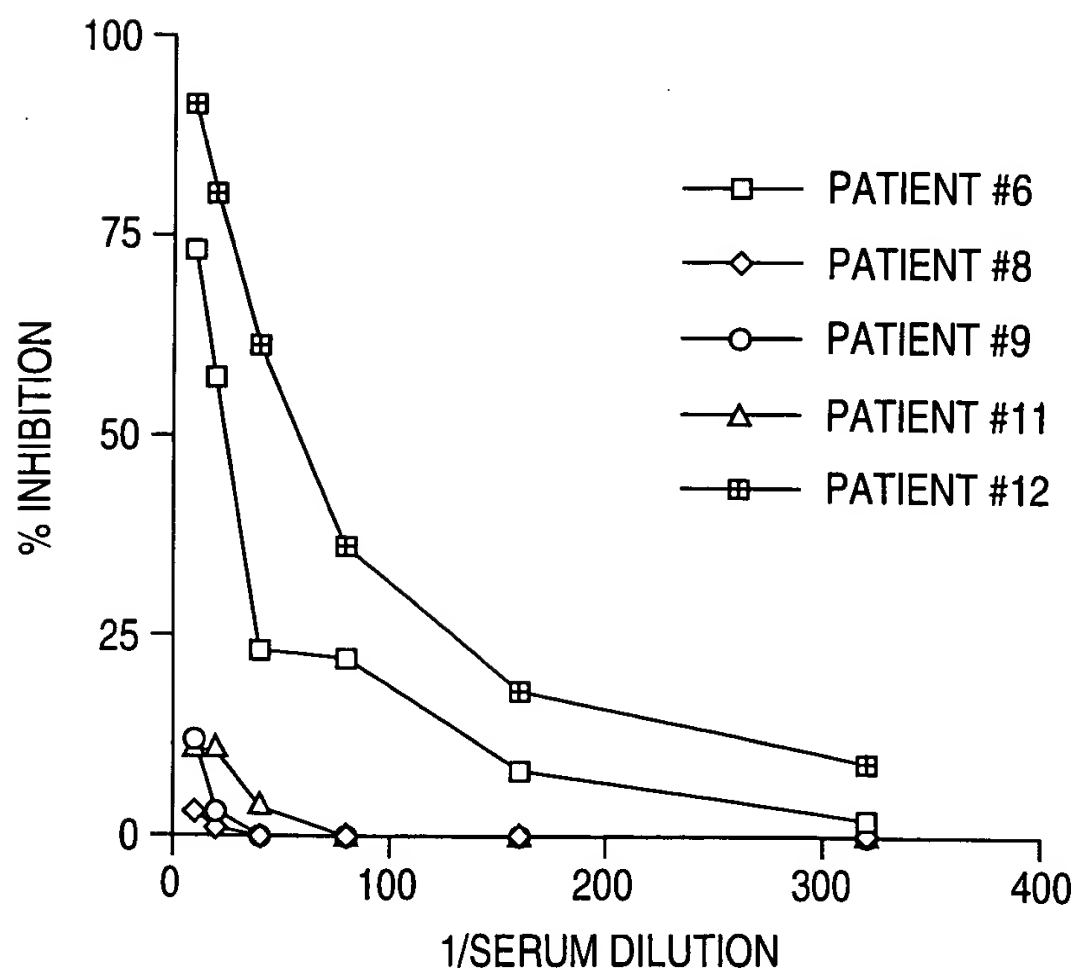


FIG. 27B

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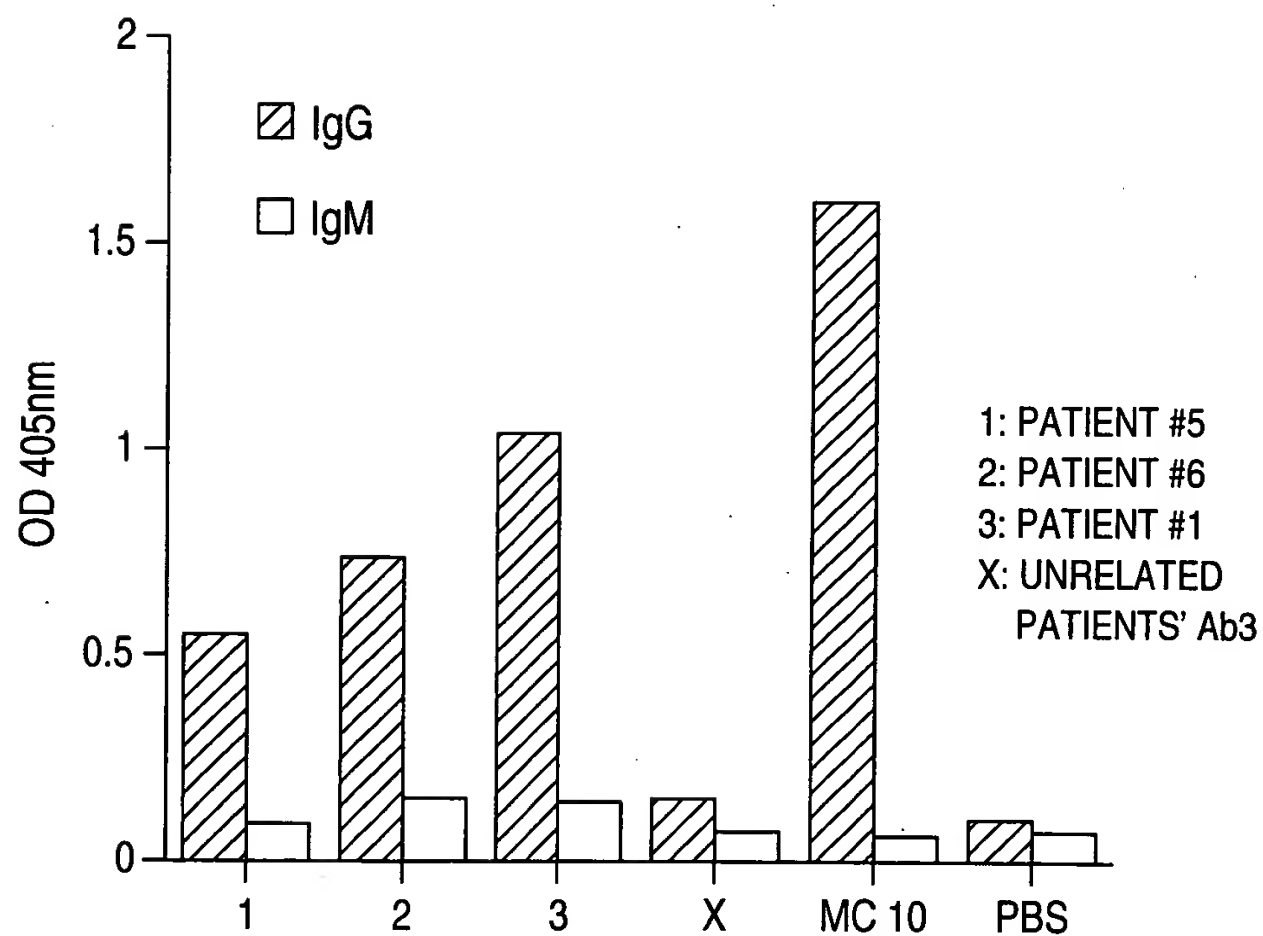


FIG. 28

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